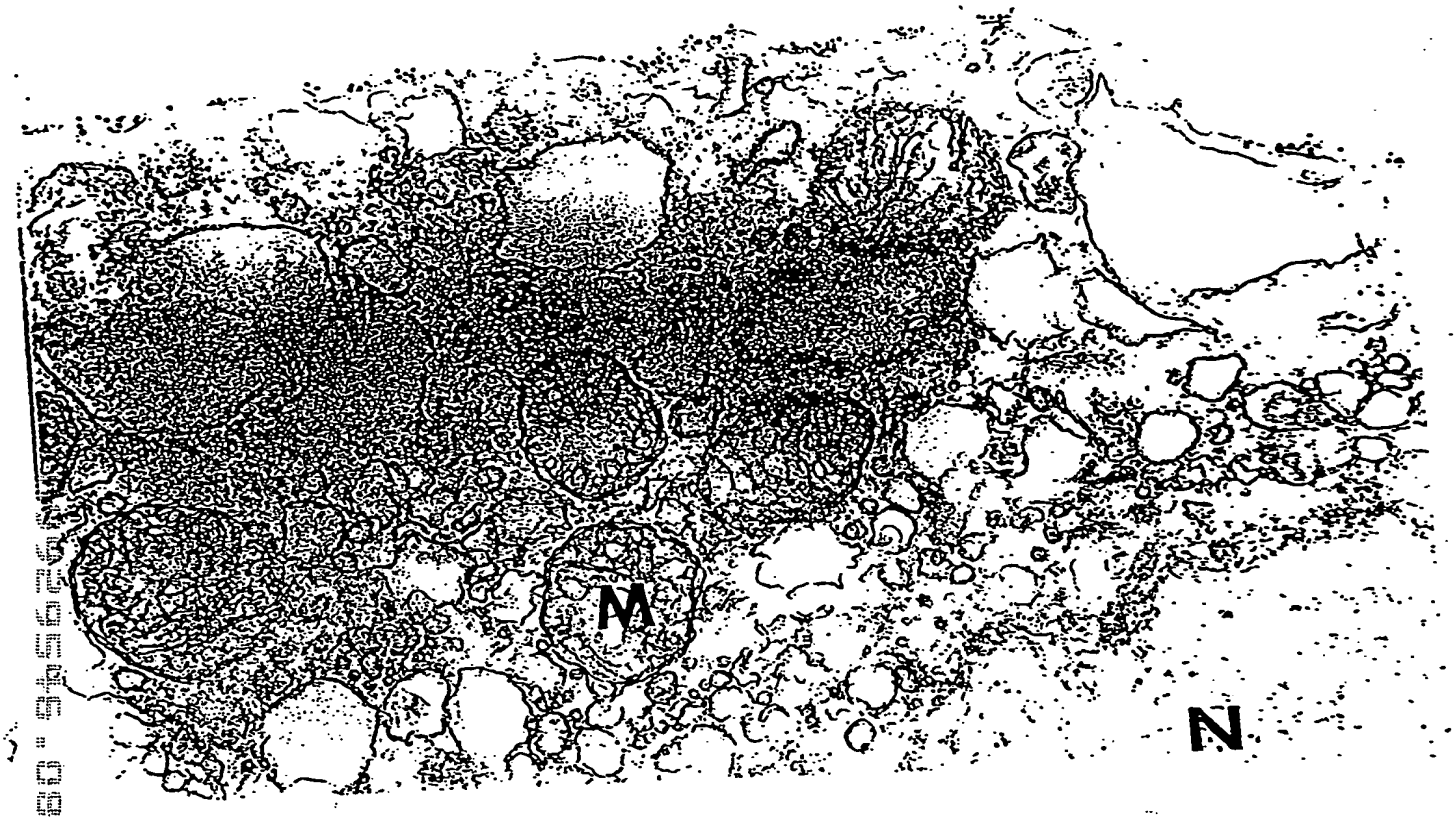

FIGURE 1

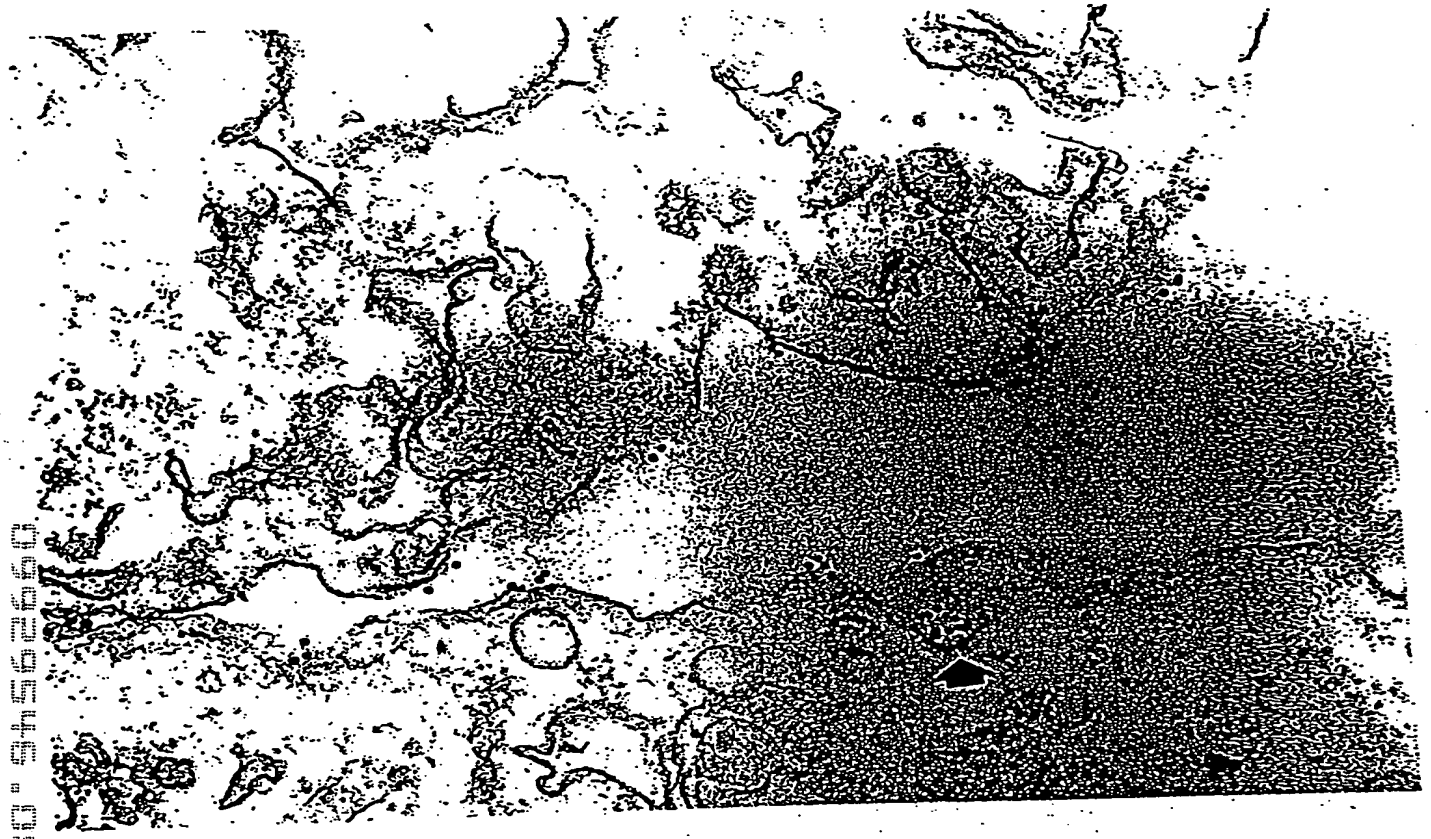

FIGURE 2

FIGURE 3

JC879 U.S. PTO
09/929546
08/13/01

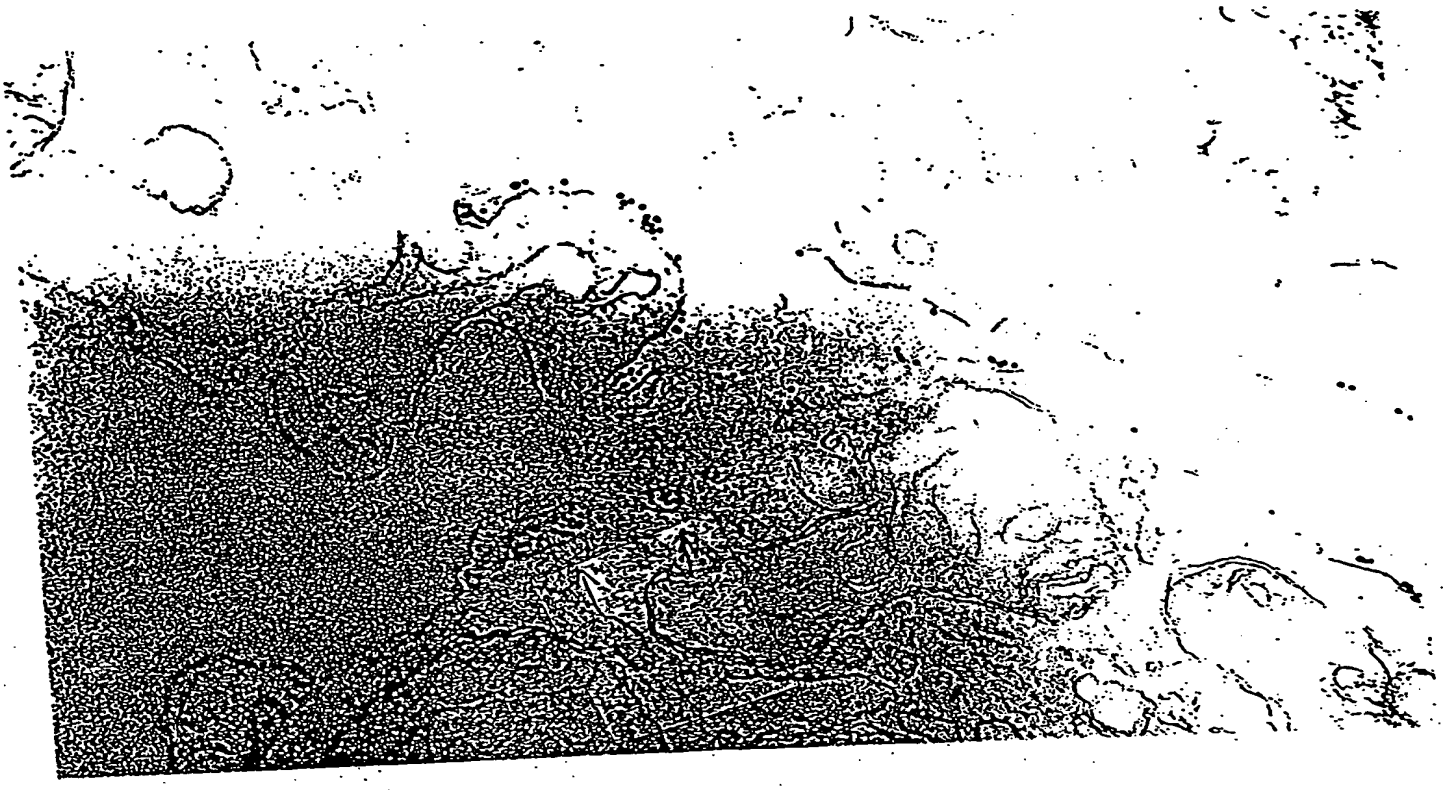

FIGURE 4

FIGURE 5

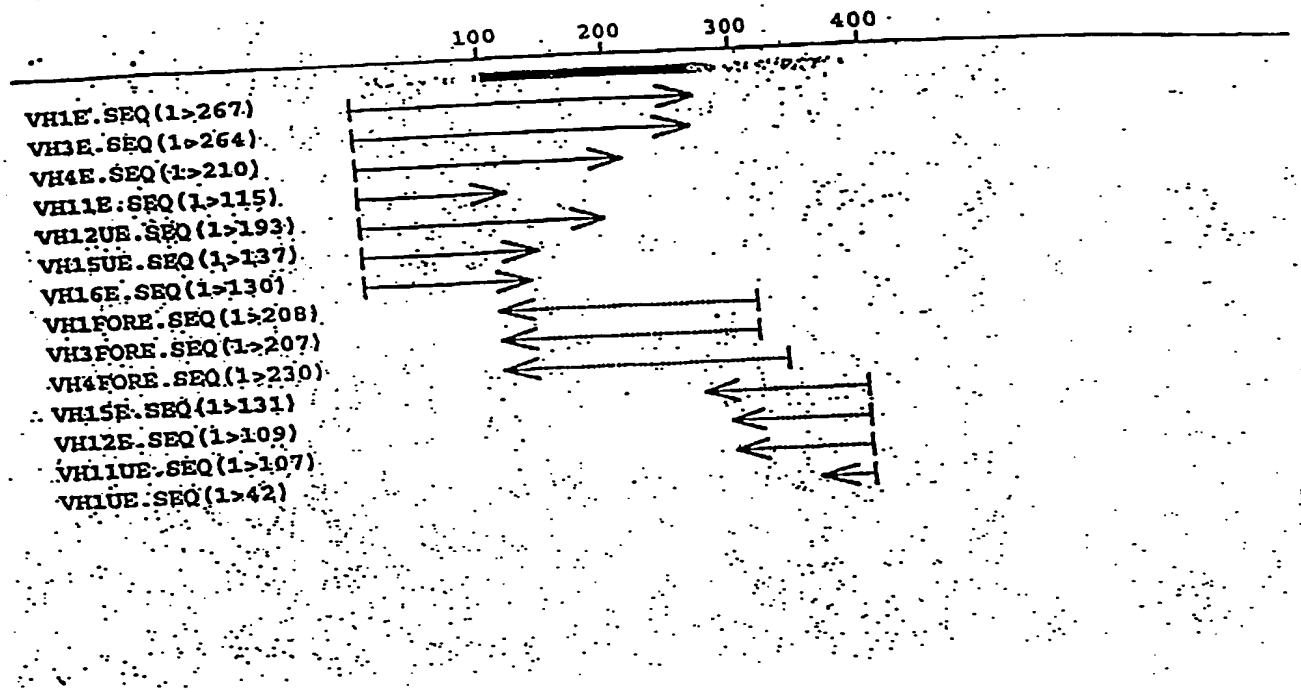
100
200
300
400
VH1E.SEQ(1>267)
VH3E.SEQ(1>264)
VH4E.SEQ(1>210)
VH11E.SEQ(1>115)
VH12UE.SEQ(1>193)
VH15UE.SEQ(1>137)
VH16E.SEQ(1>130)
VH1FORE.SEQ(1>208)
VH3FORE.SEQ(1>207)
VH4FORE.SEQ(1>230)
VH15E.SEQ(1>131)
VH12E.SEQ(1>109)
VH11UE.SEQ(1>107)
VH1UE.SEQ(1>42)

FIGURE 6

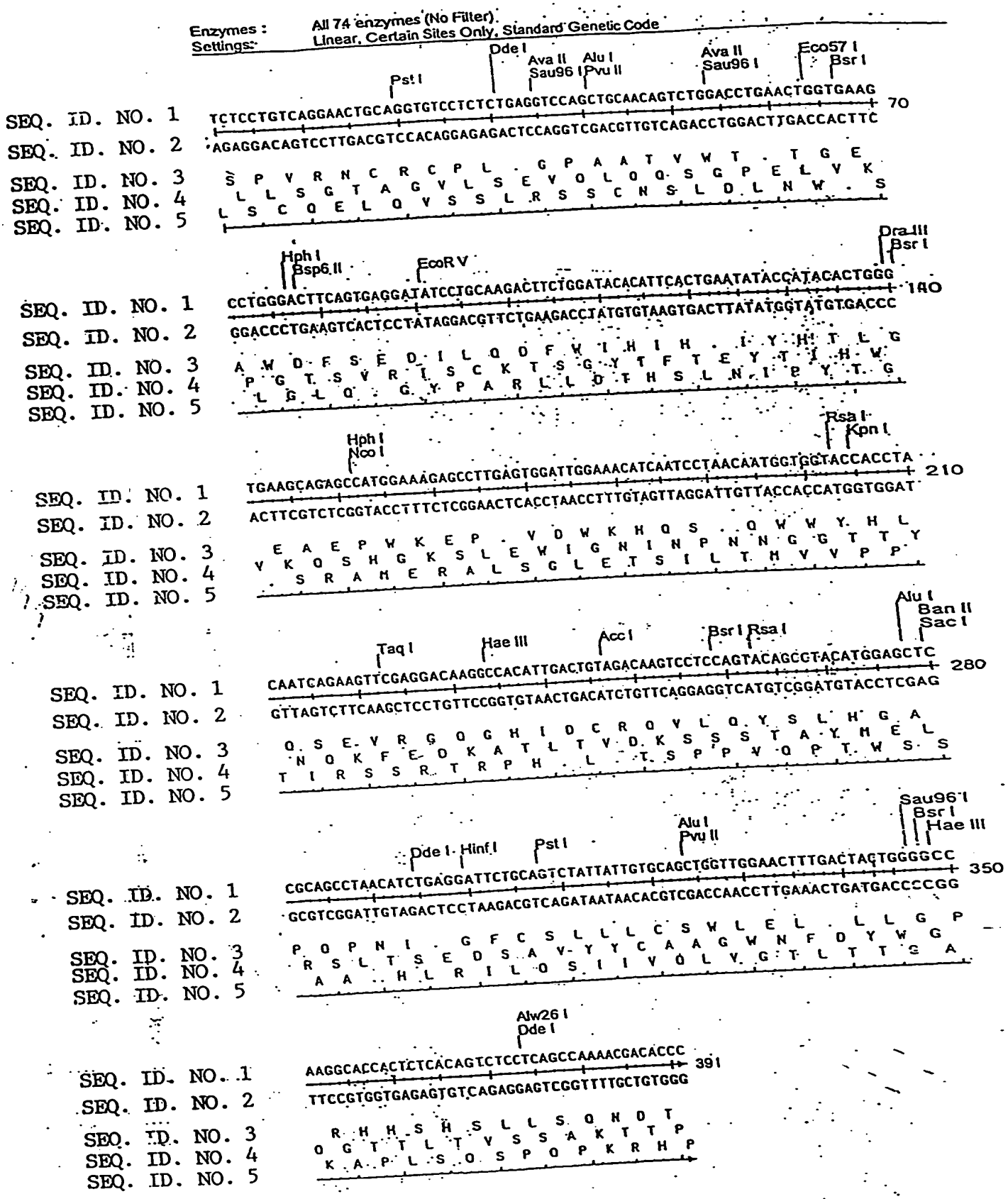
Enzymes : All 74 enzymes (No Filter).
Settings: Linear, Certain Sites Only, Standard Genetic Code
Pst I
Dde I
Ava II Sau96 I
Alu I Pvu II
Ava II Sau96 I
Eco57 I Bsr I
SEQ. ID. NO. 1
SEQ. ID. NO. 2
SEQ. ID. NO. 3
SEQ. ID. NO. 4
SEQ. ID. NO. 5
Hph I Bsp6 II
EcoR V
Dra III Bsr I
Hph I Nco I
Rsa I Kpn I
Taq I
Hae III
Acc I
Bsr I Rsa I
Alu I Ban II Sac I
Dde I Hinf I
Pst I
Alu I Pvu II
Sau96 I Bsr I Hae III
Alw26 I Dde I

FIGURE 7

Lipman-Pearson Protein Alignment
Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>115)	Seq2(1>125)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VH.PRO	MUVHIIA.PRO	75.6	2	10	125
(1>115)	(1>125)				

```
                10        20        30        40        50
EVQLQQSGPELVKPGTSVRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGGTT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y  : :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNNWVKQSPGKSLEWIGDINPGNGGTS-
                10        20        30        40        50        60

                                                  100       110
      60        70        80        90
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG--------WNFDYWGQGTT
YNQKF .KATLTVDKSSSTAYM:L SLTSEDSAVYYCA G          FDYWGQGTT
YNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGTT
      70        80        90        100       110       120

LTVSS
:TVSS
VTVSS
```

FIGURE 8

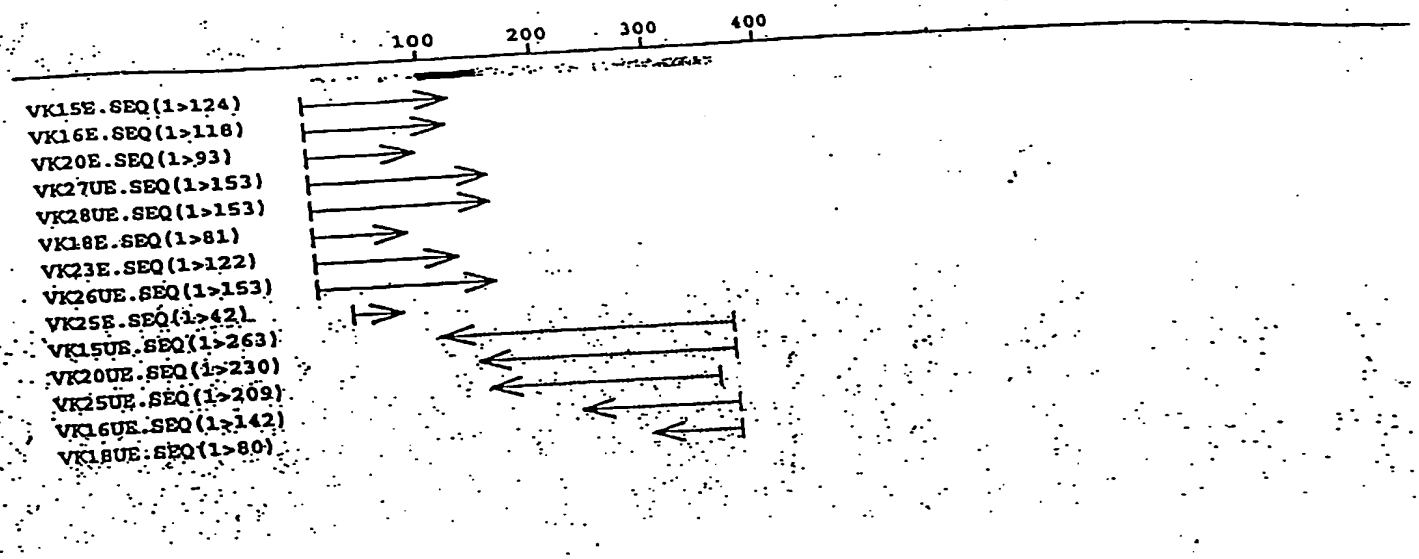
100
200
300
400
VK15E.SEQ(1>124)
VK16E.SEQ(1>118)
VK20E.SEQ(1>93)
VK27UE.SEQ(1>153)
VK28UE.SEQ(1>153)
VK18E.SEQ(1>81)
VK23E.SEQ(1>122)
VK26UE.SEQ(1>153)
VK25E.SEQ(1>42)
VK15UE.SEQ(1>263)
VK20UE.SEQ(1>230)
VK25UE.SEQ(1>209)
VK16UE.SEQ(1>142)
VK18UE.SEQ(1>80)

FIGURE 9

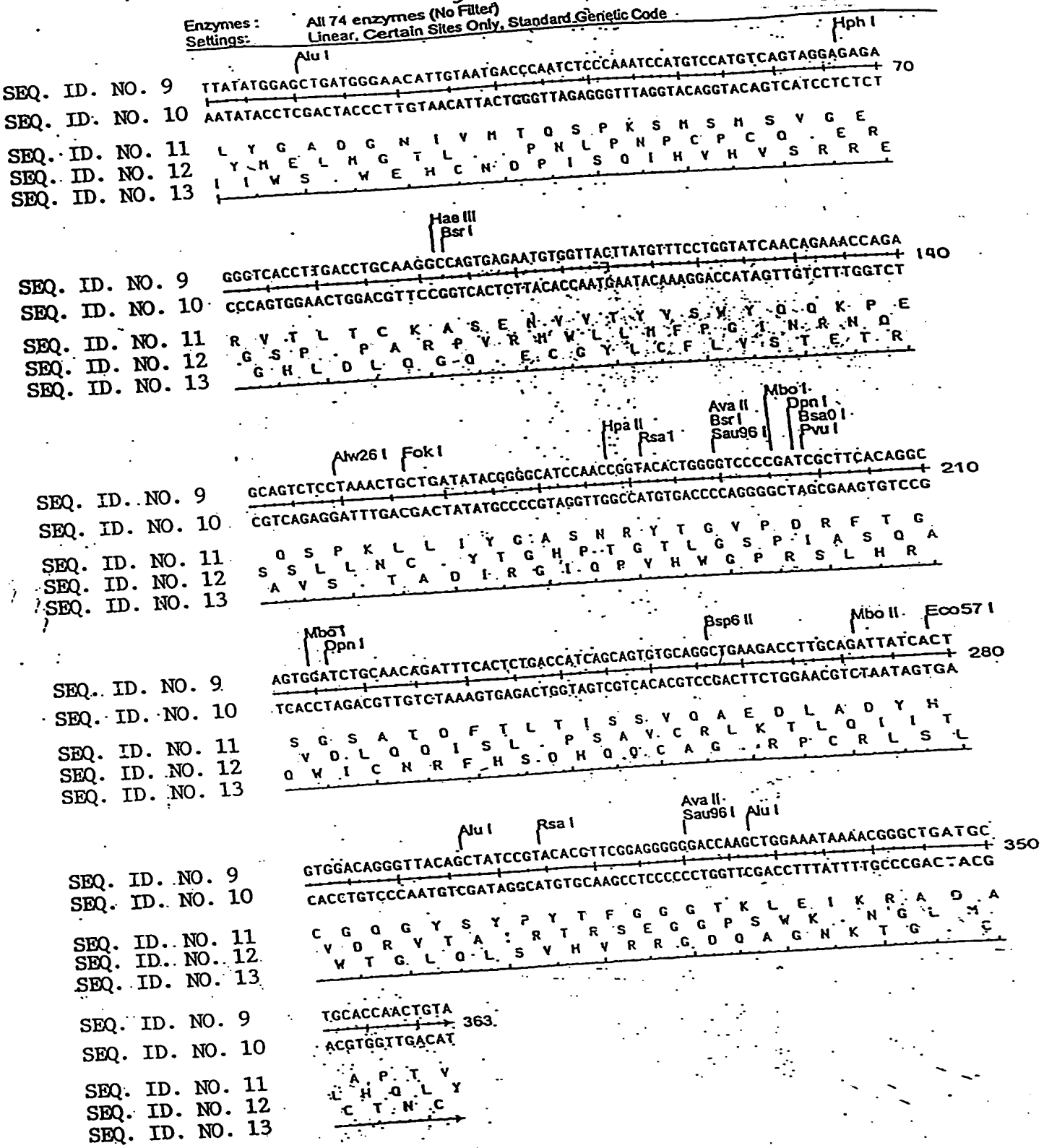
Enzymes: All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code
Hph I
Alu I
SEQ. ID. NO. 9
SEQ. ID. NO. 10
SEQ. ID. NO. 11
SEQ. ID. NO. 12
SEQ. ID. NO. 13
Hae III
Bsr I
Hpa II
Rsa I
Ava II
Bsr I
Sau96 I
Mbo I
Dpn I
Bsa0 I
Pvu I
Alw26 I
Fok I
Mbo I
Dpn I
Bsp6 II
Mbo II
Eco57 I
Alu I
Rsa I
Ava II
Sau96 I
Alu I
TGCACCAACTGTA
363
ACGTGGTTGACAT

FIGURE 10

Lipman-Pearson Protein Alignment
Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>107) J591VK.PRO	Seq2(1>111) MUVKV.PRO	Similarity Index	Gap Number	Gap Length	Consensus Length
(1>107)	(1>109)	60.4	2	2	109

```
                 10        20        30        40        50
NIVMTQSPKSMSMSVGERVTLTCKAS-ENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVP
:I MTQSP.S:S S:G:RVT:TC.AS ::: .Y::WYQQKP. SPKLLIY AS. .:GVP
DIQMTQSPSSLSASLGDRVTITCRASQDDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP
          10        20        30        40        50        60

 60        70        80        90       100
DRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSY-PYTFGGGTKLEIK
 RF GSGS TD :LTIS : : ED:A.Y C.QG : P TFGGGTKLEIK
SRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPPRTFGGGTKLEIK
          70        80        90       100
```

FIGURE 11

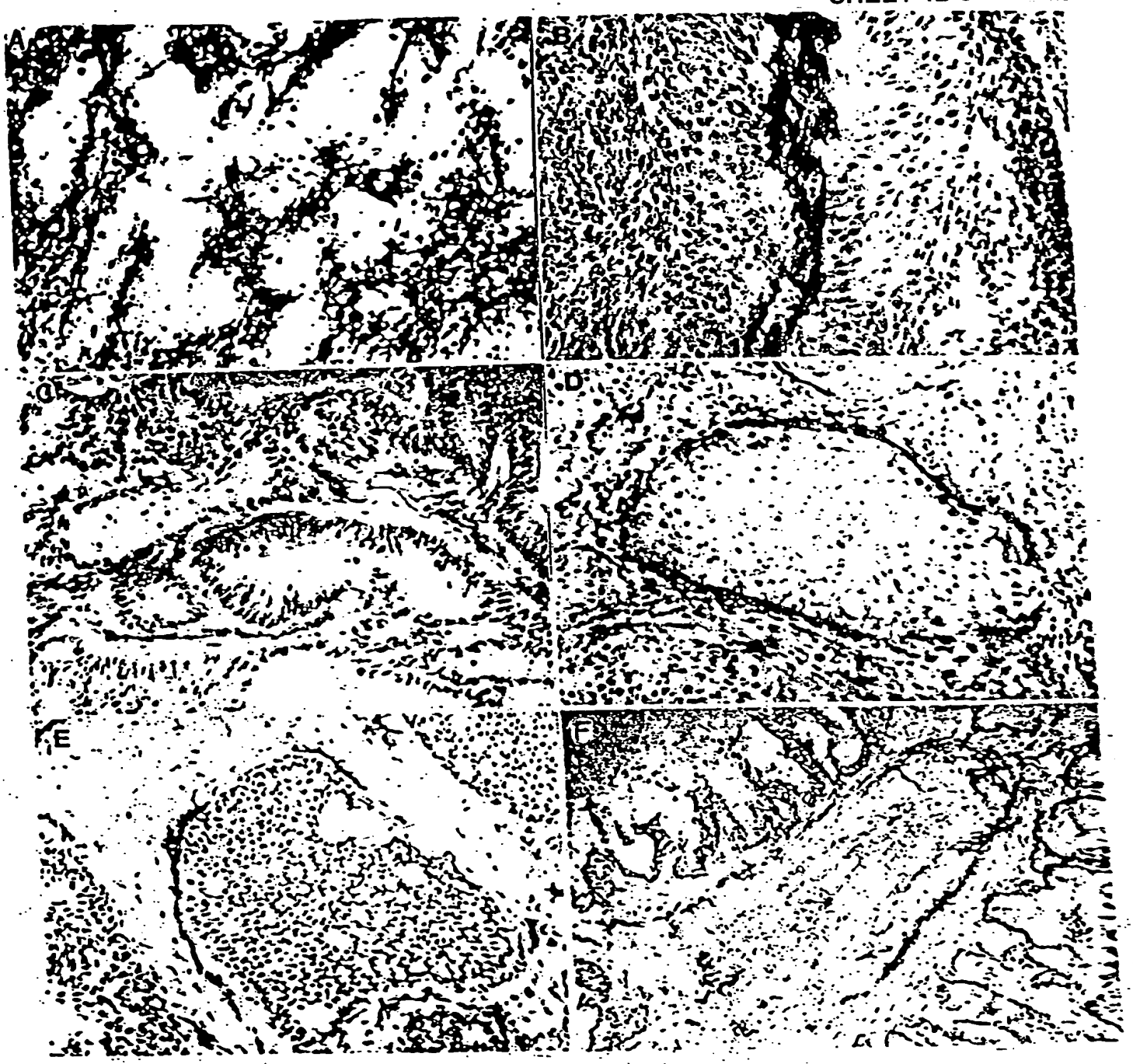

FIGURE 12